

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:08:00 ; Search time 28.8 Seconds
(without alignments)
2701.975 Million cell updates/sec

Title: US-09-911-513-2
Perfect score: 2738
Sequence: 1 MKRDHHHHQDKTMMNEE.....MLGWHRLPLIATSAWKLSTN 532

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues 473505
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTRMBL17.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Description
1	2758	100.0	023724 arabidopsis
2	2754	99.9	023643 arabidopsis
3	2747.5	99.6	031078 arabidopsis
4	2189.5	79.4	023642 arabidopsis
5	2185.5	79.2	09slh3 arabidopsis
6	2179.5	79.0	023725 arabidopsis
7	1602.5	58.1	09st48 zea mays (m
8	1595	57.8	09mb96 oryza sativ
9	1594	57.8	023759 trifolium ae
10	1587	57.5	09c8y3 arabidopsis
11	1581	57.3	065367 arabidopsis
12	1552.5	56.3	09srp9 arabidopsis
13	1490	54.0	09lf53 arabidopsis
14	967.5	35.1	09as97 oryza sativ
15	608.5	22.1	09avk4 pisum sativ
16	602.5	21.8	09m384 arabidopsis
17	598.5	21.7	096304 arabidopsis
18	590.5	21.4	09ld17 arabidopsis
19	590.5	21.4	09fuz7 zea mays (m

20	588.5	21.3	10 Q9CAN3	658	10 Q9CAN3	Q9can3 arabidopsis
21	565.5	20.5	10 Q9LPR8	482	10 Q9LPR8	Q9lpr8 arabidopsis
22	564	20.4	10 Q9S7H5	413	10 Q9S7H5	Q9s7h5 arabidopsis
23	562.5	20.4	10 Q9LPT0	526	10 Q9LPT0	Q9lpt0 arabidopsis
24	561.5	20.4	10 Q9ZSP2	428	10 Q9ZSP2	Q9zsp2 lycopersico
25	531.5	19.3	10 Q9ZTB1	313	10 Q9ZTB1	Q9ztb1 zea mays (m
26	521.5	18.9	10 Q9LWU9	617	10 Q9LWU9	Q9lwu9 oryza sativ
27	511.5	18.5	10 Q9PHZ1	405	10 Q9PHZ1	Q9fhz1 arabidopsis
28	509.5	18.5	10 Q9ZWC5	445	10 Q9ZWC5	Q9zwc5 arabidopsis
29	506.5	18.4	10 Q9XE53	306	10 Q9XE53	Q9xe53 arabidopsis
30	503.5	18.3	10 Q9ARF6	447	10 Q9ARF6	Q9arf6 capsella ru
31	487.5	17.7	10 Q9SDQ3	593	10 Q9SDQ3	Q9sdq3 arabidopsis
32	481.5	17.5	10 Q9LNX6	1502	10 Q9LNX6	Q9lnx6 arabidopsis
33	477.5	17.3	10 Q9LTI5	610	10 Q9LTI5	Q9lti5 arabidopsis
34	473	17.2	10 Q9FL03	584	10 Q9FL03	Q9fl03 arabidopsis
35	453.5	16.4	10 Q9XE58	808	10 Q9XE58	Q9xe58 arabidopsis
36	451.5	16.4	10 Q9XE51	352	10 Q9XE51	Q9xe51 arabidopsis
37	440	16.0	10 Q9L074	1336	10 Q9L074	Q9l074 arabidopsis
38	431	15.6	10 Q9XE57	284	10 Q9XE57	Q9xe57 arabidopsis
39	429	15.6	10 Q9S566	375	10 Q9S566	Q9s566 arabidopsis
40	428	15.5	10 Q9SNB8	583	10 Q9SNB8	Q9snb8 arabidopsis
41	422.5	15.3	10 Q9SCR0	542	10 Q9SCR0	Q9scr0 arabidopsis
42	418.5	15.2	10 Q9M0M5	287	10 Q9M0M5	Q9m0m5 arabidopsis
43	412	14.9	10 Q9XE52	325	10 Q9XE52	Q9xe52 arabidopsis
44	407	14.8	10 Q9O933	718	10 Q9O933	Q9o933 arabidopsis
45	393.5	14.3	10 Q9SZF7	531	10 Q9SZF7	Q9szf7 arabidopsis

ALIGNMENTS

RESULT	1
023724	
ID	023724 PRELIMINARY; PRT; 532 AA.
AC	023724;
DT	01-JAN-1998 (TREMBLrel. 05, Created)
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE	GAI PROTEIN.
GN	GAI.
OS	Arabidopsis thaliana (Mouse-ear cross).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX	NCBI_TaxID=3702;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=LANDSBERG RECTA;
RX	MEDLINE=98051192; PubMed=9389651;
RA	Peng J., Carol P., Richards D.E., King K.E., Cowling R.J.,
RA	Murphy G.P., Harberd N.P.;
RT	"The Arabidopsis GAI gene defines a signaling pathway that negatively
RT	regulates gibberellin responses.";
RL	Genes Dev. 11:3194-3205(1997).
DR	EMBL; Y15193; CAA75492.1; .
DR	Mendel; 24070; Arath.3051;24070.
SQ	SEQUENCE 532 AA; 58789 MW; 4AF4BC6EC4265503 CRC64;

Query Match 100.0%; Score 2758; DB 10; Length 532;
Best Local Similarity 100.0%; Pred. No. 8e-204;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKRDHHHHQDKTMMNEEDDNGMDLAVLGKVRSSSEMADVAQKLEQLEVMMSNVQ	60
Db	1	MKRDHHHHQDKTMMNEEDDNGMDLAVLGKVRSSSEMADVAQKLEQLEVMMSNVQ	60
QY	61	EDDLSQLATETVHYNPAELYTWLDSMLTDLNPFSSNAEYDLKAIIPGDAILNQFAIDSASS	120
Db	61	EDDLSQLATETVHYNPAELYTWLDSMLTDLNPFSSNAEYDLKAIIPGDAILNQFAIDSASS	120
QY	121	SNQGGGDDYTTNKRKCSNGVYVETTTATAESTRHVVLVDSSQNGVRLVHALLACAEVQ	180

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Db 121 SNOGGGGDTYTNKRKCSNGVVTETTTATAESTRHVVLVDSQENGVRVLLHALLACAEVQ 180
Qy 181 KENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARIYRLSPSQSPIDHSLSDTLQM 240
Db 181 KENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARIYRLSPSQSPIDHSLSDTLQM 240
Qy 241 HYEETCPYLKFAHTTANQAILAEAFQGGKRVHVVDIFSMSGQLQWPAALALRPGGPPVF 300
Db 241 HYEETCPYLKFAHTTANQAILAEAFQGGKRVHVVDIFSMSGQLQWPAALALRPGGPPVF 300
Qy 301 RLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLADSMLELRPSEIE 360
Db 301 RLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLADSMLELRPSEIE 360
Qy 361 SVAVNSVFELHKLGRPGAIDKVLGVVNOIKPEIFTVVVEQESNNHNSPIFLDRFTESLHY 420
Db 361 SVAVNSVFELHKLGRPGAIDKVLGVVNOIKPEIFTVVVEQESNNHNSPIFLDRFTESLHY 420
Qy 421 STLFDSLEGVSPGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 480
Db 421 STLFDSLEGVSPGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 480
Qy 481 HIGSNAFQAASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLSTN 532
Db 481 HIGSNAFQAASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLSTN 532
RESULT 2
O23643 PRELIMINARY; PRT; 532 AA.
ID O23643
AC O23643
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE REG2 PROTEIN.
GN REG2
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97379310; PubMed=9237632;
RA "Truong H.N., Caboche M., Daniel-Vedele F.;
RT "Sequence and characterization of two Arabidopsis thaliana cDNAs
RT isolated by functional complementation of a yeast gln3 gdh1 mutant.";
RL FEBS Lett. 410:213-218(1997).
DR EMBL; Y11337; CAA72178.1; -;
DR Mendel; 24146; Arath; 3051; 24146.
SQ SEQUENCE 532 AA; 58789 MW; 17AC719CA8072239 CRC64;

Query Match 99.9%; Score 2754; DB 10; Length 532;
Best Local Similarity 99.8%; Pred. No. 1.6e-203;
Matches 531; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRDHHHHQDKKTTMMNEEDDGNMDELLAVLGKYKRSSEMADVAQKLEQLEVMMSNVQ 60
Db 1 MKRDHHHHQDKKTTMMNEEDDGNMDELLAVLGKYKRSSEMADVAQKLEQLEVMMSNVQ 60
Qy 61 EDDLSQLATETVHYPAELYTWLDSMLTDLNPPSSNAEYDLKAIPGDAILNQFAIDSASS 120
Db 61 EDDLSQLATETVHYPAELYTWLDSMLTDLNPPSSNAEYDLKAIPGDAILNQFAIDSASS 120
Qy 121 SNOGGGGDTYTNKRKCSNGVVTETTTATAESTRHVVLVDSQENGVRVLLHALLACAEVQ 180
Db 121 SNOGGGGDTYTNKRKCSNGVVTETTTATAESTRHVVLVDSQENGVRVLLHALLACAEVQ 180
Qy 181 KENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARIYRLSPSQSPIDHSLSDTLQM 240
Db 181 KENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARIYRLSPSQSPIDHSLSDTLQM 240
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Qy 241 HYEETCPYLKFAHTTANQAILAEAFQGGKRVHVVDIFSMSGQLQWPAALALRPGGPPVF 300
Db 241 HYEETCPYLKFAHTTANQAILAEAFQGGKRVHVVDIFSMSGQLQWPAALALRPGGPPVF 300
Qy 301 RLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLADSMLELRPSEIE 360
Db 301 RLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLADSMLELRPSEIE 360
Qy 361 SVAVNSVFELHKLGRPGAIDKVLGVVNOIKPEIFTVVVEQESNNHNSPIFLDRFTESLHY 420
Db 361 SVAVNSVFELHKLGRPGAIDKVLGVVNOIKPEIFTVVVEQESNNHNSPIFLDRFTESLHY 420
Qy 421 STLFDSLEGVSPGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 480
Db 421 STLFDSLEGVSPGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 480
Qy 481 HIGSNAFQAASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLSTN 532
Db 481 HIGSNAFQAASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLSTN 532
RESULT 3
O9LQT8 PRELIMINARY; PRT; 533 AA.
ID O9LQT8
AC O9LQT8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE F10B6.34.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M.,
RA Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,
RA Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S.,
RA Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G.,
RA Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
RT I.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsy N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thavari A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006917; AAF79228.1; -;
SQ SEQUENCE 533 AA; 58926 MW; 6464B8C129D79528 CRC64;

Query Match 99.6%; Score 2747.5; DB 10; Length 533;
Best Local Similarity 99.8%; Pred. No. 5.1e-203;
Matches 532; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MKRDHHHHQDKKTTMMNEEDDGNMDELLAVLGKYKRSSEMADVAQKLEQLEVMMSNV 59
Db 1 MKRDHHHHQDKKTTMMNEEDDGNMDELLAVLGKYKRSSEMADVAQKLEQLEVMMSNV 60
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QY 60 QEDDLSQATATVHYNPAELYTWLDSMLTDLNPPSSNAEYDYLKAI PGDAILNQFAIDSAS 119
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Db 61 QEDDLSQATATVHYNPAELYTWLDSMLTDLNPPSSNAEYDYLKAI PGDAILNQFAIDSAS 120
|||||
QY 120 SSNOGGGGDTYTNKRLKCSNGVETTTATAESTRHVVLVDSQENGVRVHALLACAEAV 179
|||||
Db 121 SSNOGGGGDTYTNKRLKCSNGVETTTATAESTRHVVLVDSQENGVRVHALLACAEAV 180
|||||
QY 180 QRENLTVAEALVKQIGFLAVSOIGAMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQ 239
|||||
Db 181 QRENLTVAEALVKQIGFLAVSOIGAMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQ 240
|||||
QY 240 MHFETCPLYKFAHTANQAILEAFQGGKRVHVIDFSMSQGLQWLPALMQALALRPGGPPV 299
|||||
Db 241 MHFETCPLYKFAHTANQAILEAFQGGKRVHVIDFSMSQGLQWLPALMQALALRPGGPPV 300
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QY 300 FRLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLELRPSEI 359
|||||
Db 301 FRLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLELRPSEI 360
|||||
QY 360 ESVAVNSVFELHKLGRPGAIDKVLGVVNVQIKPEIFTVVVEQESNHNPSIFLDRFTESLHY 419
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Db 361 ESVAVNSVFELHKLGRPGAIDKVLGVVNVQIKPEIFTVVVEQESNHNPSIFLDRFTESLHY 420
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QY 420 YSTLFDSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 479
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Db 421 YSTLFDSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 480
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QY 480 AHIGSNAPKQASMLLALFNGEGYRVESDGCMLGWHTRPLIATSAWKLSN 532
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Db 481 AHIGSNAPKQASMLLALFNGEGYRVESDGCMLGWHTRPLIATSAWKLSN 533
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RESULT 4
O23642 PRELIMINARY; PRT; 587 AA.
ID O23642
AC O23642
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE RGAL PROTEIN.
GN RGAL
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97379310; PubMed=9237632;
RA Truong H.N., Caboche M., Daniel-Vedele F.;
RT "Sequence and characterization of two Arabidopsis thaliana cDNAs
RT isolated by functional complementation of a yeast gln3 gdh1 mutant.";
RL FEBS Lett. 410:213-218(1997).
DR EMBL; Y11336; CAA72177.1;
DR Mendel; 24145; Arath;3051;24145.
SQ SEQUENCE 587 AA; 64023 MW; D0A7A3C741FB51EF CRC64;
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Query Match 79.4%; Score 2189.5; DB 10; Length 587;
Best Local Similarity 74.5%; Pred. No. 5e-160;
Matches 441; Conservative 39; Mismatches 43; Indels 69; Gaps 9;
QY 1 MKRDHHH-----HH-----QDKKTMNMNEEDDNGM-DELLAVLGKVRSSSEMA 43
|||||
Db 1 MKRDHHQFQGRLSNHGTSSSSSSSISKDKMMVKKEEDGGNMDDELLAVLGKVRSSSEMA 60
|||||
QY 44 DVAQKLEQLEVMNSVQEDDLSQATATVHYNPAELYTWLDSMLTDLNPP-----SSN--- 96
|||||
Db 61 EVALKLEQLEVMNSVQEDGLSHLATDTVHYNPSELYSWLDNMLSELNPPPLPASSNGLD 120
|||||
QY 97 -----ABYDYLKAI PGDAILNQFAIDSASSNQGGGGTYYTNKRLK-CSN-- 140
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Db 121 PVLSPETICGPPASDYDLKVI PGNAIYQFPADSSSSN-----NONKRLKSCSPD 172
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QY 141 -----GW-----ETTATAESTRHVVLVDSQENGVRVHALLACAEAV 179
|||||
Db 173 SWVTSTGTGTOGGVIGTIVTTTTTAAAESTRSVILVDSQENGVRVHALLACAEAI 232
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QY 180 QRENLTVAEALVKQIGFLAVSOIGAMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQ 239
|||||
Db 233 QONNLTVAEALVKQIGCLAVSQAGAMRKVATYFAEALARRIYRLSPQONQIDHCLSDTLQ 292
|||||
QY 240 MHFETCPLYKFAHTANQAILEAFQGGKRVHVIDFSMSQGLQWLPALMQALALRPGGPPV 299
|||||
Db 293 MHFETCPLYKFAHTANQAILEAFQGGKRVHVIDFSMSQGLQWLPALMQALALRPGGPP 352
|||||
QY 300 FRLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLELRPSEI 359
|||||
Db 353 FRLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANSIADLDASMLELRPSDT 412
|||||
QY 360 ESVAVNSVFELHKLGRPGAIDKVLGVVNVQIKPEIFTVVVEQESNHNPSIFLDRFTESLHY 419
|||||
Db 413 EAVAVNSVFELHKLGRPGGIEKVLGVVVKQIKPVFTVVVEQESNHNPGVFLDRFTESLHY 472
|||||
QY 420 YSTLFDSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 479
|||||
Db 473 YSTLFDSLEGVPSQDKVMSEVYLGKQICNLVACDGPDRVERHETLSQWRNRFSGGLAP 532
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QY 480 AHIGSNAPKQASMLLALFNGEGYRVESDGCMLGWHTRPLIATSAWKLSN 531
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Db 533 AHIGSNAPKQASMLLALFNGEGYRVESDGCMLGWHTRPLIATSAWKLSN 584
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RESULT 5
O9SLH3 PRELIMINARY; PRT; 587 AA.
AC O9SLH3
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PUTATIVE RGAL, GIBBERELLIN RESPONSE MODULATION PROTEIN.
GN AT2G01570.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV: COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ranning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome II of Arabidopsis thaliana.";
RL Nature 402:761-768(1999).
DR EMBL; AC005560; AAC67333.1;
SQ SEQUENCE 587 AA; 64035 MW; FC92E7F9408072AA CRC64;
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Query Match 79.2%; Score 2185.5; DB 10; Length 587;
Best Local Similarity 74.3%; Pred. No. 1e-159;
Matches 440; Conservative 39; Mismatches 44; Indels 69; Gaps 9;
QY 1 MKRDHHH-----HH-----QDKKTMNMNEEDDNGM-DELLAVLGKVRSSSEMA 43
|||||
Db 1 MKRDHHQFQGRLSNHGTSSSSSSSISKDKMMVKKEEDGGNMDDELLAVLGKVRSSSEMA 60
|||||
QY 44 DVAQKLEQLEVMNSVQEDDLSQATATVHYNPAELYTWLDSMLTDLNPP-----SSN--- 96
|||||
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Db 61 EVALKLEQLETMNSVQEDGLSHLATDVTVHYNPSELVSWLDMNLSLPPPLPASSNGLD 120
QY 97 -----AYDLKAIPGDAILNQFAIDSASSSSNOGGGGDTYTNKRLK-CSN-- 140
Db 121 PVLSPSICGPPASDYDLKVIPIGNALYQFPALDSSSSN-----NONKRLKSCSPD 172
QY 141 -----GVV-----ETTATAESTRHVVLVDSQENGVRVHALLACAEAV 179
Db 173 SWMTSTGTGTOIGGVIGTIVTTTTTTAAAGESTRSVILVDSQENGVRVHALLACAEAI 232
QY 180 OKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSPIDHLSLDTLQ 239
Db 233 QONNLTAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSPIDHLSLDTLQ 292
QY 240 MHFETCPYLKFAHFTANQALILEAFQGGKRVHVIDFSMSQGLQWALMALRPGGPPV 299
Db 293 MHFETCPYLKFAHFTANQALILEAFQGGKRVHVIDFSMSQGLQWALMALRPGGPPV 352
QY 300 FRLTGIGPPAPDNFDYLVHVGCKLAHLAEATHVEFEYRGFVANSIADLADSMLELRPSDT 359
Db 353 FRLTGIGPPAPDNFDYLVHVGCKLAHLAEATHVEFEYRGFVANSIADLADSMLELRPSDT 412
QY 360 ESVAVNSVFEHLKLLGRPGAIDKVLGVVYNQIKPELFTVVEQESNHNPIFLDRFTESLHY 419
Db 413 EAVAVNSVFEHLKLLGRPGAIDKVLGVVYNQIKPELFTVVEQESNHNPIFLDRFTESLHY 472
QY 420 YSTLFDLSLEGVPQSKVMSEVYLGKQICNVVACDPDRVERHETLSQWRNRFSGAGFAA 479
Db 473 YSTLFDLSLEGVPQSKVMSEVYLGKQICNVVACDPDRVERHETLSQWRNRFSGAGFAA 532
QY 480 AHIGSNAPKQASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLST 531
Db 533 AHLGNSAPKQASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLST 584

RESULT 6
Q23725 PRELIMINARY; PRT; 587 AA.
ID O23725
AC O23725
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GRS PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Peng J., Carol P., Richards D.E., King K.E., Cowling R.J.,
RA Murphy G.P., Harberd N.P.;
RL Genes Dev. 0:0-0(0).
DR EMBL; Y15194; CAA75493.1; -
DR Mendel; 24071; Arath:3051.24071.
SQ SEQUENCE 587 AA; 64006 MW; F6F6C7738EE7DCA9 CRC64;

Query Match 79.0%; Score 2179.5; DB 10; Length 587;
Best Local Similarity 74.0%; Pred. No. 3e-159;
Matches 438; Conservative 41; Mismatches 44; Indels 69; Gaps 9;
QY 1 MKRDHHH-----HH-----QDKKTMNNEEDDNGCM-DELLAVLGKYKVRSSBMA 43
Db 1 MKRDHHQFQGRLSNHTSSSSSSISKDKMMVMVKKEDGGNMDDELLAVLGKYKVRSSBMA 60
QY 44 DVAOKLEQLEVMNSVQEDDLSQATETVHYNPAELTYWLDMLTDLNPP-----SSN--- 96
Db 61 EVALKLEQLETMNSVQEDGLSHLATDVTVHYNPSELVSWLDMNLSLPPPLPASSNGLD 120
QY 97 -----AYDLKAIPGDAILNQFAIDSASSSSNOGGGGDTYTNKRLK-CSN-- 140

Db 121 PVLSPSICGPPASDYDLKVIPIGNALYQFPALDSSSSN-----NONKRLKSCSPD 172
QY 141 -----GVV-----ETTATAESTRHVVLVDSQENGVRVHALLACAEAV 179
Db 173 SWMTSTGTGTOIGGVIGTIVTTTTTTAAAGESTRSVILVDSQENGVRVHALLACAEAI 232
QY 180 OKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSPIDHLSLDTLQ 239
Db 233 QONNLTAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSPIDHLSLDTLQ 292
QY 240 MHFETCPYLKFAHFTANQALILEAFQGGKRVHVIDFSMSQGLQWALMALRPGGPPV 299
Db 293 MHFETCPYLKFAHFTANQALILEAFQGGKRVHVIDFSMSQGLQWALMALRPGGPPV 352
QY 300 FRLTGIGPPAPDNFDYLVHVGCKLAHLAEATHVEFEYRGFVANSIADLADSMLELRPSDT 359
Db 353 FRLTGIGPPAPDNFDYLVHVGCKLAHLAEATHVEFEYRGFVANSIADLADSMLELRPSDT 412
QY 360 ESVAVNSVFEHLKLLGRPGAIDKVLGVVYNQIKPELFTVVEQESNHNPIFLDRFTESLHY 419
Db 413 EAVAVNSVFEHLKLLGRPGAIDKVLGVVYNQIKPELFTVVEQESNHNPIFLDRFTESLHY 472
QY 420 YSTLFDLSLEGVPQSKVMSEVYLGKQICNVVACDPDRVERHETLSQWRNRFSGAGFAA 479
Db 473 YSTLFDLSLEGVPQSKVMSEVYLGKQICNVVACDPDRVERHETLSQWRNRFSGAGFAA 532
QY 480 AHIGSNAPKQASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLST 531
Db 533 AHLGNSAPKQASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLST 584

RESULT 7
Q9ST48 PRELIMINARY; PRT; 630 AA.
ID Q9ST48
AC Q9ST48
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE GIBBERELLIN RESPONSE MODULATOR (FRAGMENT).
GN DB.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99347734; PubMed=10421366;
RA Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,
RA Flintham J.E., Beales J., Fish L.J., Worland A.J., Pellica F.,
RA Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;
RT "Green revolution" genes encode mutant gibberellin response
RT modulators.*;
RL Nature 400:256-261(1999).
DR EMBL; AJ242530; CAB51557.1; -
DR NON_TER 630 630
SQ SEQUENCE 630 AA; 66028 MW; 3D56851726C51042 CRC64;

Query Match 58.1%; Score 1602.5; DB 10; Length 630;
Best Local Similarity 54.0%; Pred. No. 8.1e-115;
Matches 344; Conservative 68; Mismatches 106; Indels 119; Gaps 15;
QY 1 MKRDHHHHHQD-----KKTMM-----NEEDDNGMDLAVLGKYKVRSSM 42
Db 1 MKRE----YDAGGSGDGMSSKDKMMAAAGAGEQEED--VDELLAALGYKVRSSDM 53
QY 43 ADVAOKLEQLEVM-----SNVQEDD--LSQATETVHYNPAELTYWLDMLTDLNPP 93
Db 54 ADVAOKLEQLEVMAMGGMGGVAGAGATDGGFVSHLATDVTVHYNPDLSSWVESMLSNAP 113
QY 94 -----SSNAEYDLKAIPGDAILNQFAI 115

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Db 114 PAPLPATPAPRLASTSSTVTSGAAGAGYFDLPPAVDSSSSSTYALKPIP-----SPVAA 168
Qy 116 DSASSNOG-----GGGDTYTTNKLKCSNG-----VVE-----TTTATAESTR-- 154
Db 169 PSADPSTDSARPKRMRTGGGTSSTSSSSSSMDGRTSSVVEAAPATQASAAANGPA 228
Qy 155 -HVVLVDSQENGVRVLVHALLACAEAVQENLTVAEALVKQIGFLAVSQIGAMRKVATYFA 213
Db 229 VPVVVVDTQEAGIRLVHALLACAEAVQENFSAEALVKQIPMLASSOGGAMRKVAAVFG 288
Qy 214 EALARIYRL--SPSQSPIDHSLDLOMHFYETCPYLKFAHFTANQAILAEAFQCKRVH 271
Db 289 EALARVYRFRPPDOSSLLDAADFLLHAHFYESCPLYKFAHFTANQAILAEAFACRVH 348
Qy 272 VIDFSNCSQLOWPALMQALALRPGPPVFRLTGIGPPADPNFYDHEVGCKLAHLAEAIH 331
Db 349 VVDFGKQGMQWPAQLQALALRPGPPSFRLTGIGVGPQDETALQVQGWKLAQFAHTR 408
Qy 332 VEFYRGFVANTLADLASMLELR-----PSEIESVAVNSVFLKHLGRPGAKIDKVLGV 387
Db 409 VDFQYRGLVAATLADLEPFMLQPEGDDTDDEPEVIANSVPELHRLLAQPGALEKVLGT 468
Qy 388 NQIKPEIETVVEQESNHNPSIFLDRFTESLHYSTLFDLSLEGVPSGQ----- 434
Db 469 RAVRPRIVTVVEQEAHNHSGTFLDRFTESLHYSTLFDLSLEGAGAGSGQSTDPASPAAG 528
Qy 435 -DKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAAAHIGSNAPKQASML 493
Db 529 TDQVMSEVYLGKQICNVVACEGATERHETLQWRSLGSGGFAPVHLGNSNAYKQASTL 588
Qy 494 LALFNGGEGYRVESDGLMLGWHPRLPIATSAWKL 530
Db 589 LALFAGGEGYRVEEKDGLTLGWHTRLPIATSAWRA 625

RESULT 8
Q9MB96 PRELIMINARY; PRT; 625 AA.
ID Q9MB96;
AC Q9MB96;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE OSGAI.
GN OSGAI.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. NIPPONBARE;
RC MEDLINE=20179680; PubMed=10713441;
RA Ogawa M., Kusano T., Katsumi M., Sano H.;
RT "Rice gibberellin-insensitive gene homolog, OSGAI, encodes a nuclear-
RT localized protein capable of gene activation at transcriptional
RT level."
RL Gene 245:21-29(2000).
DR EMBL; AB030956; BAA90749.1; -.
SQ SEQUENCE 625 AA; 65406 MW; 034FF02719D42E97 CRC64;
```

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Query Match 57.8%; Score 1595; DB 10; Length 625;
Best Local Similarity 56.08; Pred. No. 3e-114;
Matches 332; Conservative 67; Mismatches 110; Indels 84; Gaps 10;

Qy 19 BEDDNGMDLAVLGKVRSEMDVAVQKLEQLEVMM-----SNVQEDLSQLATE 70
Db 34 EEDD---VDLEALALGKVRSSMDVAVQKLEQLEMAMGVSAPGAADDGFGVSHLATD 90
Qy 71 TVHYNPAELYTWLDSMLTDLNP----- 94
Db 91 TVHYNPSDLSSWVESMLSELNAPLPIPPAPPAARHASTSSTVTGGGGGFELPAAADS 150
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Qy 95 SNAEYDLK--AIPGDAILNOFAIDSASSN--OGGGDTYTTNKLKCSNG-----VVE 144
Db 151 SSSYIALRPISLPVVATADPSAASARDTKRMRTGGGTSSTSSSSSSSLGGGASRGSVVE 210
Qy 145 TTTATAESTR-----HVVLVDSQENGVRVLVHALLACAEAVQENLTVAEALVKQIGFL 197
Db 211 AAPPATCGAAAAANAPVPVVVDTQEAGIRLVHALLACAEAVQENFAAAEALVKQIPTL 270
Qy 198 AVSQIGAMRKVATYFAEALARIYRLSPSQSP-IDHSLDLOMHFYETCPYLKFAHFTA 256
Db 271 AASOGGAMRKVAAVFEALARVYRFRPADSTLLDAADFLLHAHFYESCPLYKFAHFTA 330
Qy 257 NOAILEAFQGGKRVHIVIDFSMSQGLQWPAQLALRPGPPVFRLTGIGPPADPNFYD 316
Db 331 NOAILEAFAGCHRVHIVDFGKQGMQWPAQLQALALRPGPPSFRLTGIGVGPQDETAL 390
Qy 317 HEVGCKLAHLAEAIHVEFYRGFVANTLADLASMLELR-----PSEIESVAVNSVFLH 371
Db 391 QOVGWKLAQFAHTRVDFQYRGLVAATLADLEPFMLQPEGADANEPEEVIANSVPELH 450
Qy 372 KLLGPPGAIDKVLGVVNOIKPEIETVVEQESNHNPSIFLDRFTESLHYSTLFDLSLEGV 431
Db 451 RLLAQPGALEKVLGTVAHVRPRIVTVVEQEAHNHSGTFLDRFTESLHYSTLFDLSLEG 510
Qy 432 SGQ-----DKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGF 477
Db 511 SQGAELSPPAAGGGGTQVMSEVYLGKQICNVVACEGATERHETLQWRNRLGRAGF 570
Qy 478 AAHIGSNAPKQASMLALFNGGEGYRVESDGLMLGWHTRLPIATSAWKL 530
Db 571 EPVHLGNSNAYKQASTLALFAGGEGYRVEEKDGLTLGWHTRLPIATSAWRA 623

RESULT 9
Q9ST59 PRELIMINARY; PRT; 623 AA.
ID Q9ST59;
AC Q9ST59;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE GIBBERELLIN RESPONSE MODULATOR.
GN RHT-DIA.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99347734; PubMed=10421366;
RA Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,
RA Flinham J.E., Beales J., Fish L.J., Worland A.J., Pellica F.,
RA Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;
RT "Green revolution" genes encode mutant gibberellin response
RT modulators."
RL Nature 400:256-261(1999).
DR EMBL; AJ242531; CAB51555.1; -.
SQ SEQUENCE 623 AA; 65337 MW; F2BAC34996D0A84F CRC64;
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Query Match 57.8%; Score 1594; DB 10; Length 623;
Best Local Similarity 54.38; Pred. No. 3.6e-114;
Matches 332; Conservative 71; Mismatches 106; Indels 102; Gaps 11;
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```
Qy 11 DKKTMMNEEDDGMDELLAVLGKVRSEMDVAVQKLEQLEVMM-----SNVQEDD- 63
Db 22 EDKMWSAAGAGEVDELLAALGYKVRASDMADVAVQKLEQLEMAMGNGVGAAPDSD 81
Qy 64 -LSQATETVHYNPAELYTWLDSMLTDLNP----- 93
Db 82 FATHLATDTVHYNPTDLSWVESMLSELNAPPPPPAPQLNASTSSTVTGGGGFYDLP 141
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[illegible]

DR	Mendel;	29006;	Arath;	3051;	29006.
DR	InterPro;	IPR001680;	WD40.		
DR	Pfam;	PF00400;	WD40;	1.	
DR	SMART;	SM00320;	WD40;	1.	
DR	PROSITE;	P550082;	WD_REPEATS_2;		
DR	PROSITE;	P550234;	WD_REPEATS_REG		
KW	Repeat;	WD repeat.			
SQL	SEQUENCE	662 AA;	73126 MW;	9	

Query Match	57.3%;	Score 1581;	DB 10;	Length 662;
Best Local Similarity	58.7%;	Pred. No. 3.9e-113;		
Matches 317; Conservative	75;	Mismatches 104;	Indels 44;	Gaps 9;

Qy	2	KROHHHHQD- - - - - KKTMMNEEDDGNMDELLAVLGVKVRSSMADVAQKLEQLEVMM	56
Db	153	QREHNHRESSAGEGGSSMTVTKKEBAAGVDELLVVLGVKVRSSMADVAHLEQLEVMYL	212
Qy	57	SNVQEDDLSQIATETVHYNPAEYLTLWDSMLTDLNP- - - - - P3SNAEYDLKAIPGDAILNQ	112
Db	213	G- - - - - DGISNLSDSETVHYNPSDL3GWVESMLSDLPTRIOEKPEYDRLAIPGSVAIYPR	268
Qy	113	FAIDSASSNQGGGGTYT- - - - - NKRLKCSNVVETTATAESTRHVVLVDSOENGVRVLVH	170
Db	269	- - - - - - - - - - - DEHYTRRSKRTEISEL- - - - - SSTRSVVLDSOETGVRLVH	305
Qy	171	ALLACAEAVOKENLTVAEALVIOGFLAVSQIGAMRKVATYFAEALARRIYRLSPSOSPI	230
Db	306	ALLACAEAVOONNLKADALVHGVGLASSOAGAMRKVATYFAEGLARRIYRIPDDVA	365
Qy	231	DHSLSDTLQMHFYETCPYLKFAHFTANQAILAEAFQKKRVHVIDFSMSOGLOWPALMQAL	290
Db	366	SSSFSDTLQTHFYESCPLYLKFAHFTANQAILAEVFAEKVHVIDLGNHGLQWALPQIAL	425
Qy	291	ALRPGGPPVRLTIGCPPADPNFDYDHEYGVCKLAHLAEAIHVEFEYRGFVANTLADLDAS	350
Db	426	ALRPGGPPDLRTIGYSLTD- - - - - TQEVGWKLCQLASTIGVNFEPK3TALNNLSDLKPE	481
Qy	351	MLELRPSETESVAVNSVFLHLKLLGRPGAIDKVLGVVNOIKPFEITVTVQESNHN3PIFL	410
Db	482	MLDIRPG-LESVAVNSVFLHLRLUHLAPHSIDKFLSTIKSIRPDDIMTVVEQEHNHGTVEL	540
Qy	411	DRETESLHYVYSTLDFSLEGVP3GQDKVMSEVYLKGOICNVACDGDPRDVERHETL3OWEN	470
Db	541	DRETESLHYVSYSLFDSLEGPP3- QDRVMSBELFLGRQLNLVACEGEDRVERHETLNQWRN	599
Qy	471	RFGSAGFAAAHIG3NAFKAQ3MALLFN3GEGYRVYEE3DGLMGLM3WHTRPLIAT3AWKL3	530
Db	600	RFLGFGFKPV3IG3NAFKAQ3MALLYAGAD3YVNEBEN3GLL3GQTR3PAT3AWRLN	659

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RESULT 12
ID Q9SRP9 PRELIMINARY; PRT; 547 AA.
Q9SRP9
Q9SRP9;
DC DT 01-WAY-2000 (TrEMBLrel. 13, Created)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
DE RGAI-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OC NCBI_TaxId=3702;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RA "Arabidopsis thaliana chromosome III BAC T21P5 genomic sequence."
RT Submitted (Oct-1999) to the EMBL/GenBank/DDJB databases

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DR EMBL; AC009895; AAF01590.1; -.
SQ SEQUENCE 547 AA; 60493 MW; C4D18D5951D95634 CRC64;

Query Match 56.3%; Score 1552.5; DB 10; Length 547;
Best Local Similarity 59.08; Pred. No. 4.5e-11;
Matches 323; Conservative 79; Mismatches 90; Indels 55; Gaps 13;

Qy	11	DKYTMNNEEDDNGM---	DELLAVLGVKYVRSSEMA	ADVAKLEQLEVMNSNQVEDDL	-SQ	66
Db	29	DKK----	KADDNNNSNMDELLAVLGVKYVRSSEMA	EAQKLEQLEWLSN---	DDVGST	81
Qy	67	LATETVHYNPAELYTWLDSMLTDLNPPSSN----	AEYDLKATPGDAILNOF--		113	
Db	82	VLDSVHYNPSDLNSWVESMLSELNPPASSDLDTTRTSCVDRSEYDURAIPG---	LSAFPK		138	
Qy	114	----	AIDSASSNSOGGGDVTYTNKRUKCSGVVETTTATAESTRHHVVLVDSQENGVRLVH		170	
Db	139	EEVFDEEASS-----	KRIRLGS----	WCESSESTRSVVLVDSQETGVRLVH	182	
Qy	171	ALLACBAVOKENLTVAEALVKGIOFLAVLSQIGAMRKVATYFAEALARRIYRLSPSQ----		227		
Db	183	ALVACAEIAHQENLNLADALVKRGVTLAGSQAGAMGKVATYFAQALARRIYRTYATADV		242		
Qy	228	-SPIDHSLSDTLOHWFYETCPYLKFAHFTANQAILAEAFQCKKRVHVIDFSMSGLOMPAL		286		
Db	243	CAAVNPSFEVLEMHFYESPYLKFAHFTANQAILAEAVTTARKRVHVIDLGLNGOMQMPAL		302		
Qy	287	MQALALRPGGPPVFRLTGIGPPAPDNFDYLHEVGCGLAHIAEAIHVEFVYRGVANTLAD		346		
Db	303	MQALALRPGGPPSFRLTGIGPPQTSNDSLSLOQLGWKLQAPFAQNMGVFEFEKGLAAESLSD		362		
Qy	347	LDSMLELRPSETESVAVNSVFLKHLGLRGAIDKVLGVVNOIKPEITFTVBQESNNHS		406		
Db	363	LEPEMETRP-ESETLVNVSFVFLHRLRLARSGSTIELLNTVKAIKPSITVTVQEANHNG		421		
Qy	407	PIELDRFTESLHYXSTLFDLSLE----	GVPSQDKVMSEVILGKIOICNVWACDGDPRVERHE		463	
Db	422	IVFLDRFNEALHYXSLFDLSLEDSYSLPS--	QDRVMSEVILGROIILNVAAEGSDRVERHE		480	
Qy	464	TLQWNRNFGSAGFAAAHIGSNFAKQASMLLALFNSEGEGYRVBESDGCGLMWLGHTRPLTIA		523		
Db	481	TAQWRIRMKSAQFDPHLHGSSAFKQASMLLSLYATCDGYRVEENDGCLMWIGWQTRPLIT		540		
Qy	524	TSAWKLS	530			
Db	541	TSAWKLA	547			

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RESULT 13
Q91F53 PRELIMINARY; PRT; 523 AA.
ID Q91F53;
AC Q91F53;
DT DT 01-OCT-2000 (trEMBLrel. 15, Created)
DT 01-OCT-2000 (trEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (trEMBLrel. 15, Last annotation update)
DE RGA-LIKE PROTEIN.
OS K3M16_60.
GN Arabidopsis thaliana (Mouse-ear cress) .
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
RP Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP EU Arabidopsis sequencing project;
RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL391150; CAC01893.1; -.
DR

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SQ SEQUENCE 523 AA; 57326 MW; 0F6CE0BD13403C35 CRC64;

Query Match 54.0%; Score 1490; DB 10; Length 523;
Best Local Similarity 57.3%; Pred. No. 2.7e-106;
Matches 315; Conservative 78; Mismatches 105; Indels 52; Gaps 14;

QY 1 MKRDHHHQDKTMMNEE--DDGNG-----MDLLAVLGKYSRSEMDVADVAQKLEQLE 53
DB 1 MKRSHOETSVEEADSMVEKLENGCGGGDDNMDDEFLAVLGKYSRSEMDVADVAQKLEQLE 60
QY 54 VMNSNVQEDDL---SQTATEVHYNPAELYTWLDSMLTDLN---PPSSNAEYDLKAIPGD 107
DB 61 MYLSN-----DASSNAFNDTVHYNPSDLSGWAQMSLDLNYPDLPNRCIDLRPIYDD 116
QY 108 AILNOFAIDASSNOGGGDTYTNKRLK-----CSNGWETTTATAESTRHVVLVDSQE 163
DB 117 -----DECCSSNS-----NSNKRILGPWCD-----SVTSESTRSVLI--EE 152
QY 164 NGVRLVHALLACAEAVQKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRL 223
DB 153 TGVRLVQALVACAEAVQLENLSLADALVKRVGLLAASQAGAMGKATYFAEALARRIYRI 212
QY 224 SPSQSPIDLSLDTLQMHFYETCPYLKFAHETANOAILAEAFQGKKRVHVIDFSMSQGLW 283
DB 213 HPSAAADPSFEELIOMFYDSCPYLKFAHETANOAILAEVTTSRVHVVIDLGNQGMOW 272
QY 284 PALMQALALRPGGPPFRFLTGTGPPAPDNFYLVHVGCKLAHLAEAIHVEFEYRGFVANT 343
DB 273 PALMQALALRPGGPPFRFLTGTGVNPS--NREGIOELGWKLAQAIGVEKFNGLTTER 330
QY 344 LAD 403
DB 331 LSDLEPDMFETR--TESETLVNVSFELHPVLSQPGSIEKLLATKAVKPLVTVVVEQBAN 389
QY 404 HNSPFLDRFTESLHYSTFLDSLEG---VPSGQDKVMSEVYLGKQICNVVACDGPDRVE 460
DB 390 HNGDVLDRFNEALHYSTFLDSLEGVYVPS--QDVMSEVYLGKQILNVLVATESDRIE 448
QY 461 RHETLSQWRNRFSGAGFAAAHIGSNAPKQASMLLALFNGEGYRVVEESDGLMLGHWTRP 520
DB 449 RHETLAQWRKMGSAFGDPVNLGSDAPKQASMLLALFNGEGYRVVEESDGLMLAQWTKP 508
QY 521 LIATSAWKLS 530
DB 509 LIAASAWKLA 518

RESULT 14

Q9AS97 PRELIMINARY; PRT; 493 AA.
AC Q9AS97;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE PUTATIVE OSGAL.
GN P0707D10.30.

OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;

QY 53 BVMSNVQEDDLSQLATETVHYNPAELYTWLDSMLTDLPSSNNEYDLKAIPGDAL--- 109
DB 344 DVWPTSLHFSDSITLNNQNNQNN--MFPNWGATQINNNNNPS---VSLVTIPSPQLSTQ 397
QY 110 -----LNQFAIDSASSNOGGGDTYTNKRLKCSNGVWTTTATAESTRHVVLVDSQ- 162
DB 398 OQOHOIQQHPEDLAPAT-----TTTSAEL-----ALARKKEEKEQKKK 440
QY 163 -ENGVRVLHALLACAEAVQKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARR-- 219
DB 441 DEEGLHLTLTLLQCAEAVSAENLEQANKMLLEISQLSPFGTSAQRVAAYFEAISARLV 500

Query Match 35.1%; Score 967.5; DB 10; Length 493;
Best Local Similarity 52.0%; Pred. No. 3.9e-66;
Matches 194; Conservative 63; Mismatches 101; Indels 15; Gaps 7;

QY 165 GVRVLHALLACAEAVQKENLTVAEALV--KQIGFLAVSQIGAMRKVATYFAEALARRLY- 221
DB 81 GIRLVHLLMSCAGAIETAGDHASLAQADLAALAAVSAASGIGRVAVHFTTALSRRLLFP 140
QY 222 -RLSPSPIDLSLDTLQMHFYETCPYLKFAHETANOAILAEAFQGKKRVHVIDFSMSQG 280
DB 141 SPVAPPTTDAEHAF---LYHHFYEACPYLKFAHETANOAILAEAFHGHCDHVVHIDSLMQG 197
QY 281 LQWPAALQALALRPGGPPFRFLTGTGPPAPDNFYLVHVGCKLAHLAEAIHVEFEYRGFV 340
DB 198 LQWPAALQALALRPGGPPFRFLTGTGPPAPDNFYLVHVGCKLAHLAEAIHVEFEYRGFV 340
QY 341 ANTLADLADLADLADLADLADLADLADLADLADLADLADLADLADLADLADLADLADLAD 397
DB 258 ANSDEVPRWMLQTAG--EAVAFNSVLQHLRLGLDPAQAPIDAVLDCVASVRPKIFTV 315
QY 398 VQESNHNPSIFLDRFTESLHYSTFLDSLEGVPS--GQDKVMSEVYLGKQICNVVACDG 455
DB 316 IEQADHNTKTGFLDRFTEALFYSAVFDLDAASGAGNAMAAYLQREICDIVCGEG 375
QY 456 PDRVERHTLSQWRNRFSGAGFAAAHIGSNAPKQASMLLALFNGEGYRVVEESDGLMLG 515
DB 376 AARREHPEPLSRWRDLTRAGLSAVPLGSLNALQOAMLVGLFS--GEGHSVEEADGCLTLG 434
QY 516 WHTRPLIATSAWK 528
DB 435 WHGRPLFSASAW 447

RESULT 15

Q9AVK4 PRELIMINARY; PRT; 819 AA.
AC Q9AVK4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE SCARECROW.
GN PSSCR.

OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Pisum.
NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ALASKA;
RA Sassa N., Matsushita Y., Nakamura T., Nyunoya H.;
RT "Molecular characterization and in situ expression pattern of pea
SCARECROW gene."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB048713; BAB39155.1;
SQ SEQUENCE 819 AA; 90372 MW; 41B67BD6DC72ADFA CRC64;

Query Match 22.1%; Score 608.5; DB 10; Length 819;
Best Local Similarity 33.4%; Pred. No. 3.5e-38;
Matches 168; Conservative 87; Mismatches 181; Indels 67; Gaps 19;

QY 53 BVMSNVQEDDLSQLATETVHYNPAELYTWLDSMLTDLPSSNNEYDLKAIPGDAL--- 109
DB 344 DVWPTSLHFSDSITLNNQNNQNN--MFPNWGATQINNNNNPS---VSLVTIPSPQLSTQ 397
QY 110 -----LNQFAIDSASSNOGGGDTYTNKRLKCSNGVWTTTATAESTRHVVLVDSQ- 162
DB 398 OQOHOIQQHPEDLAPAT-----TTTSAEL-----ALARKKEEKEQKKK 440
QY 163 -ENGVRVLHALLACAEAVQKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARR-- 219
DB 441 DEEGLHLTLTLLQCAEAVSAENLEQANKMLLEISQLSPFGTSAQRVAAYFEAISARLV 500


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QY 220 -----IYRLSP--SOSPIDHSLSDTLQMHFYETCPYLKFAHFTANQAILEAFQGGKRRVHV 272
Db 501 SSCLGIYATLPVSSHPTPHNQKVASAFQV-FNGISPFVKFSHTANCAIQEAFEREERVHI 559
QY 273 IDFSMSOGLQWPAALRGCGPPVFRLTGIGPPADPNFDYLHEVGCKLAHLAEAIHV 332
Db 560 IDLDIMQGLQWPLGHEHILASRPGGPPYVRLTGLG----TSMETLEATGKRLSDFANKLGL 615
QY 333 EFYRGF-VANTLADLDASMLELRPSEIESVAVNSVFELHKLGRPGAIDKVLGVVNOIK 391
Db 616 PEEF--FPAEKVGNIDVEKLVN--SKSEAVAVH--WLQHSLYDVTGSDTNTLWLLQRLA 569
QY 392 PEFTVVEQESNHNSPIFLDRETESLHYSTLFDL---EGVPSGQDKVMSEVYLGKQIC 448
Db 670 PKVTVVEQDLS-NAGSFLGREVEAIHYYSALFDSLGSYGSESEERHVVEQQLLSREIR 728
QY 449 NVVACDGDPR---VERHETLSQWRNRFGSAGFAAAHIGSGNAFKQASMLLALFNGGEGYRV 505
Db 729 NVLAVGGFSRSGEIRFH----NWREKLOCCGFRGVSLAGNATQASLLIGMF-PSEGYTL 783
QY 506 EESDGLMLGLWHTRPLIATSAMK 528
Db 784 VEDNGILKLGWKDLCILLTASAWR 806

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Job time: 212 sec

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